



SEQUENCE LISTING

<110> MacPhee, Colin Houston
Tew, David Graham
Southan, Christopher Donald
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Gloger, Israel Simon
Lawrence, Geoffrey Mark Prouse
Rice, Simon Quentyn John

<120> Lipoprotein Associated Phospholipase A2,
Inhibitors Thereof and Use of the Same in Diagnosis and
Therapy

<130> P30693C4X1C1

<140> 09/922,067

<141> 2001-08-03

<150> 09/193,130

<151> 2000-11-28

<150> 08/387,858

<151> 1994-06-24

<150> PCT/GB94/01374

<151> 1994-06-24

<150> GB 9313144.9

<151> 1993-06-25

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 37

<212> PRT

<213> Homo sapien

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1				5				10					15		
Ser	Asn	Lys	Ala	Ser	Leu	Ala	Phe	Leu	Gln	Lys	His	Leu	Gly	Leu	His
			20					25					30		
Lys	Asp		Phe	Asp	Gln										
					35										

<210> 2

<211> 30

<212> PRT

<213> Homo sapien

<400> 2

Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro

1	5	10	15
Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn			
20	25	30	

<210> 3
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20 25	

<210> 4
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<400> 4	
Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr	
1 5 10 15	
Pro Ala Asn	

<210> 5
 <211> 420
 <212> DNA
 <213> Homo sapien

<220>
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 <222> 265, 390, 395, 403, 406
 <223> n = A,T,C or G

<400> 5	
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gtgttgattg gttgtgttaa tgttggtccc tggaataaga ttctcatcat ctccttcaat 120	
caagcagtc cactgatcaa aatctttatg aagtcctaaa tgcttttgta agaatgctaa 180	
tgaagctttg ttgctaagat caatagctgc atttgaatct atgtctccct ttaatttgag 240	
catgtgtcca attattttgc cagtngcaaa agtgaagtca gcaaaattct ggtggactga 300	
acccttgatt gtaatcatct ttctttcttt atcaggtgag tagcattttt tcatttttat 360	
gatattagca ggatattgga aatattcagn gttgntaaaa agnggnggct gagggattct 420	

<210> 6
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 <212> DNA
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<220>
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 <222> 84

<223> n = A,T,C or G

<400> 6

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aatcaggggt tcagtccacc aganttttgc tgacttccact tttgcaactg gcaaaaataat 120
tggaacacatg ctcaaattaa agggagacat agattcaaatt gtagctattg atcttagcaa 180
caaagcttca ttagcattct taaaaaagca tttaggactt cataaagatt ttgttcagtg 240
ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300
caattcaaca catcatgttt acagaacttc ttccaggga taggaggaaa tacaattggg 360
gtttaaaata gggtttttt 379
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<210> 7

<211> 279

<212> DNA

<213> Homo sapien

<220> Feature

<221> misc_feature

<222> 257

<223> n = A,T,C or G

<400> 7

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aaaaatagca gtaattggac attcttttgg tggagcaacg gttattcaga ctcttagtga 120
agatcagaga ttcagatgtg gtattgccct ggatgcatgg atgtttccac tgggtgatga 180
agtatatcc agaattcctc agcccctctt ttttatcaac tctgaatatt tccaatatcc 240
tgctaataatc ataaaantgg aaaaatgcta ctcacctgg 279
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<210> 8

<211> 572

<212> DNA

<213> Homo sapien

<400> 8

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gatcagagat tcagatgtgg tattgccctg gatgcatgga tgtttccact ggggtgatgaa 120
gtatatccca gaattcctca gccctctttt tttatcaact ctgaatattt ccaatatcct 180
gctaatatca taaaaatgaa aaaatgctac tcacctgata aagaaagaaa gatgattaca 240
atcaggggtt cagtcacca gaattttgct gacttccact ttgcaactgg caaaataatt 300
ggacacatgc tcaaattaaa gggagacata gattcaaatt tagctattga tcttagcaac 360
aaagcttcat cagcattctt acaaaagcat ttaggacttc ataaagattt tgatcagtgg 420
gactgcttga ttgaaggaga tgatgagaat cttattccag ggaccaacat taacacaacc 480
aatcaacaca tcatgttaca gaactcttca ggaatagaga aatacaatta ggattaaaat 540
agggtttttta aaaaaaaaaa aaaaaaaact cg 572
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<210> 9

<211> 1361

<212> DNA

<213> Homo sapien

<400> 9

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tcctgttgcc catatgaaat catcagcatg ggtcaacaaa atacaagtac tgatggctgc 180
tgcaagcttt ggccaaaacta aaatcccccg gggaaatggg ctttattccg ttggttgtag 240
agacttaatt tttgatcaca ctaataaggg caccttcttg cgtttatatt atccatccca 300
agataatgat cgccttgaca ccctttggat cccaaataaa gaatattttt ggggtcttag 360
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caaatttctt ggaacacact ggcttatggg caacattttg aggttactct ttggttcaat 420
gacaactcct gcaaactgga attcccctct gaggcctggg gaaaaatata cacttggtgt 480
tttttctcat ggtcttgggg cattcaggac actttattct gctattggca ttgacctggc 540
atctcatggg tttatagttg ctgctgtaga acacagagat agatctgcat ctgcaactta 600
ctatttcaag gaccaatctg ctgcagaaat aggggacaag tcttggctct accttagaac 660
cctgaaacaa gaggaggaga cacatatacg aaatgagcag gtacggcaaa gagcaaaaga 720
atgttcccaa gctctcagtc tgattcttga cattgatcat ggaaagccag tgaagaatgc 780
attagattta aagtttgata tggaacaact gaaggactct attgataggg aaaaaatagc 840
agtaattgga cattcttttg gtggagcaac gggtattcag actcttagtg aagatcagag 900
attcagatgt ggtattgccc tggatgcatg gatgtttcca ctgggtgatg aagtatatc 960
cagaattcct cagcccctct tttttatcaa ctctgaatat ttccaatatc ctgctaatat 1020
cataaaaaatg aaaaaatgct actcacctga taaagaaaga aagatgatta caatcagggg 1080
ttcagtccac cagaattttg ctgacttcac ttttgcaact ggcaaaataa ttggacacat 1140
gctcaaatta aagggagaca tagattcaaa tgcagctatt gatcttagca acaaagcttc 1200
attagcattc ttacaaaagc atttaggact tcataaagat tttgatcagt gggactgctt 1260
gattgaagga gatgatgaga atcttattcc agggaccaac attaacacaa ccaatcaaca 1320
catcatgtta cagaactctt caggaataga gaaatacaat t 1361

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<210> 10
<211> 7
<212> PRT
<213> Homo sapien

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<400> 10
Gln Tyr Ile Asn Pro Val Ala
 1                5

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<210> 11
<211> 20
<212> PRT
<213> Homo sapien

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<400> 11
Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr
 1                5                10                15
Phe Ala Thr Gly
          20

```

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<210> 12
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<212> PRT
<213> Homo sapien

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<400> 12
Gln Tyr Ile Asn Pro Ala Val
 1                5

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<210> 13
<211> 5
<212> PRT
<213> Homo sapien

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<400> 13

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Gln Tyr Ile Asn Pro
1 5

<210> 14
<211> 441
<212> PRT
<213> Homo sapien

<400> 14

Met Val Pro Pro Lys Leu
1 5

His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe
10 15 20

Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp
25 30 35

Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr
40 45 50

Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu
55 60 65 70

Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro
75 80 85

Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu
90 95 100

Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly Thr His Trp Leu Met Gly
105 110 115

Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr Pro Ala Asn Trp
120 125 130

Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser
135 140 145 150

His Gly Leu Gly Ala Phe Arg Thr Leu Tyr Ser Ala Ile Gly Ile Asp
155 160 165

Leu Ala Ser His Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg
170 175 180

Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp Gln Ser Ala Ala Glu Ile
185 190 195

Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr Leu Lys Gln Glu Glu Glu
200 205 210

Thr His Ile Arg Asn Glu Gln Val Arg Gln Arg Ala Lys Glu Cys Ser
215 220 225 230

Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp His Gly Lys Pro Val Lys
235 240 245

Asn Ala Leu Asp Leu Lys Phe Asp Met Glu Gln Leu Lys Asp Ser Ile
 250 255 260
 Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr
 265 270 275
 Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala
 280 285 290
 Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile
 295 300 305 310
 Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala
 315 320 325
 Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser Pro Asp Lys Glu Arg Lys
 330 335 340
 Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr
 345 350 355
 Phe Ala Thr Gly Lys Ile Ile Gly His Met Leu Lys Leu Lys Gly Asp
 360 365 370
 Ile Asp Ser Asn Ala Ala Ile Asp Leu Ser Asn Lys Ala Ser Leu Ala
 375 380 385 390
 Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln Trp Asp
 395 400 405
 Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu Ile Pro Gly Thr Asn Ile
 410 415 420
 Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly Ile Glu
 425 430 435
 Lys Tyr Asn
 440